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RAW SEQUENCE LISTING DATE: 06/21/2002 PATENT APPLICATION: US/09/940,925A TIME: 12:20:02

Input Set : A:\Seqsub2.app

SEQUENCE LISTING

Output Set: N:\CRF3\06212002\I940925A.raw

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(1) GENERAL INFORMATION:
             (i) APPLICANT: BROW, MARY ANN D.
      6
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                            LYAMICHEV, VICTOR I.
      8
                            OLIVE, DAVID M.
            (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
     10
                                      PATHOGENS
     11
           (iii) NUMBER OF SEQUENCES: 165
     13
            (iv) CORRESPONDENCE ADDRESS:
     15
                  (A) ADDRESSEE: MEDLEN & CARROLL
     16
                  (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
     17
     18
                  (C) CITY: SAN FRANCISCO
                  (D) STATE: CALIFORNIA
     19
                  (E) COUNTRY: UNITED STATES OF AMERICA
     20
     21
                  (F) ZIP: 94104
             (V) COMPUTER READABLE FORM:
     23
                  (A) MEDIUM TYPE: Floppy disk
     24
     25
                  (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     26
     27
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     29
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/940,925A
C--> 30
C--> 31
                  (B) FILING DATE: 10-Jun-2002
     32
                  (C) CLASSIFICATION:
          (viii) ATTORNEY/AGENT INFORMATION:
     34
     35
                  (A) NAME: CARROLL, PETER G.
                  (B) REGISTRATION NUMBER: 32,837
     36
                  (C) REFERENCE/DOCKET NUMBER: FORS-01756
     37
     39
            (ix) TELECOMMUNICATION INFORMATION:
                  (A) TELEPHONE: (415) 705-8410
     40
                  (B) TELEFAX: (415) 397-8338
     41
        (2) INFORMATION FOR SEQ ID NO: 1:
     44
             (i) SEQUENCE CHARACTERISTICS:
     46
     47
                  (A) LENGTH: 2506 base pairs
     48
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
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     50
                  (D) TOPOLOGY: linear
     52
            (ii) MOLECULE TYPE: DNA (genomic)
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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     62 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC
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70 GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGACGGCT ACGAGGTCCG CATCCTCACC 72 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCACC CCCCGAGGGG 73 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCACCC CCCCGAGGGG 74 GACTACCAGG CCCTCACCGG GCTCTGGGAA AAGTACGGCC TGAGGCCCGA CCCGTGGGCC 75 GACTACCGGG CCCTGACCGG GACAGCTC GACAACCTTC CCGGGGTCAA GGGCATCGGG 76 GACTACCGGG CTGAGCCCG CATCCGGGAA AAGTACGGCC TGGAAGCCCT CCTCAAAGAAC 77 GCTCTCCTGGGA ACCTGGCCAA GCTGCGCACC GACAACCTGG CCCACATGGA CGATCTGAAG 75 CTCTCCTCGG ACCTGGCCAA GCTGCGCACC GACCTCCCC TGGAAGCCCT CCTCAAAGAAC 76 CTCTCCACG ACTTCGGCAA GCTTCGGGAA AAGATCCTGG CCCACATGGA CGATCTGAAG 77 CTCTCCACG ACTTCGGCCAA GCTTCGGCACA GCTTTCTGCCAAA AGAGCCCTGA GCTTCACCAAA 78 CACACCCCC AGCGCAAGCCC TTCTCGGCA AGAGCCCTGA GCTTTCACCCAAA 78 CCCCCCAGAG GGCCTTCTG GCCTTTCTGCCC AAGAGCCCCTA GTGTGGCCCCA 78 CCCCTCAGGA ACCTCAAAGAA GCCCTTTTCTGCCA AAGAACCCTAC GCTTCTTGGC 79 CTTCTGGCCA ACCACCACCC CAAGGGGGG CTCTCTCGCC AAGAACCCTAC CCTTCTTGGC 70 CTCTTGGCCA ACACCACCCC CAAGGGGGG CTCTCTCGCA AAGAACCCTAC CCTTCTTGGC 70 CAGGGGGAAG ACCGCCCCCCCCGC AAGACCCCAA AGAACCCTAC CCTTCTTGGC 70 CAGGGGGGAA GCCGGCCCC CCTTTCCAGA AGACCCTCAC CTCCTCCTCGC 70 CAGGGGGGAAGACCGCCC CCTTTCCAGA AGACCCTAC CCTACCTTCTG 70 CAGGGGGAAGAACCCCCCCCTCT CACCCCCCCCCCCCC											
22 GCGACAAAG ACCTTTACCA GCTCCTTCC GACCCATCC ACCCCCAGGGG											
74 TRCCTCATCA CCCCGGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCGA CCACTGGGCC 76 GACTACCGGG CCCTGACCGG GACCAGTCC GACAACCTTC CCGGGTCTAA GGGCATCGGG 77 GACTACCGGG CCCTGACCGG GACCAGTCC GACCAACCTTC CCGGGTCTAA GGCATCGGG 80 CTGGACCAGC TCTGGAGGAA TGGGGGAGCC TGGAAGCCTC CCTCAACAAC 81 CTGCACCGGC TAAACCCGC CATCCGGGAA AAGATCCTGC CCCACATGGA GATTTGAAC 82 CTCTCCTGGG ACCTGGCCAA GGGGCCCCC TGGAGGGGCA CTGCCCAA 83 AGGCGGAGC CCGACCGGCA GAGGCTTAGG GCCTTCTTG AGAGGCTGA GTTTGGCCAA 84 AGGCGGAAC CCGACCGGCA GAGGCTTAGG GCCTTTCTGG AGAGGCCCC TGGAGGAGC CCCTGGCCC 900 85 CCCCCGGAAG GGCCTTCGT GGCTTTTCTGC TCTTCCCCACA AGAGCCCCAT GTGGCCGAT 90 CTTCTGGCAA GAGGCCTTCGT GGCTTTCTGC TCTTCCCCACA AGAGCCCCAT GTGGCCGAT 91 CTTCTGGCAA GAGGCCTTCGT GGCTTTCTGC AAGAGCCCAT GTGGCCCAT GTGGCCGAT 92 CCCTCAAGG ACCTGAAGGA GGCGCGGGGG CGGTCCACC GGCCCCCA GCTTATAAA 1020 92 CCCTCAAGG ACCTGAAGGA GGCCGCGGGG CTTCTCCCCA AGAACCTGAG CGTTCTGCC 90 CACCCTTCCA ACACCACCCC CCAGGGGGG CGGCCCCCA ACGACCTGA CGCTTCTCCA 96 GACCCTTCCAA ACACCACCCC CCAGGGGGG CGCCCCCCTTCCCCA AGACCTGAG CGTTCTCCC 97 CACCCTTCCAA CACCCACCCC CCAGGGGGT GCCCGGCGCT ACGCCGGGA TGGACCAT 96 GACCCTTCCAA ACACCACCCC CCAGGGGGT GCCCGGCGCT ACGCCGGGA TGGACCAT 96 CACCCTTCCAA ACACCACCCC CCAGGGGGT GCCCGGCGCT ACGCCGGGA TGGACCAT 100 GAGGGGGAG AGAGCCTCC TTGCCCTTTCCCAA AGACCTCATC GGCAGGCTT 100 CAGGGGGAA GAGGCTCCT TTGCCTTTAC CCGCAGCTG ACGCCCCAT GCAGGCCTT 100 CTGGCCCACA TGGAGCCAC GGGGGTGCC CTGGACGTGG CTTTCCACCT GCCAGGCCT 100 CTGCCCCACA TGGAGCCAC GGGCGTCCC CTGGACGTGG CTTTCCACCT GCCAGGCCT 101 CCCCTCCCGC AGGCCCAC CCTTCCCCG GAACACGGA AAGACGTCC CACCCCAGACG CTTCCACCAC GCCCCACCC CCCCCCCCCC											
6 ACTACCAGGE CCACACACCAG GACCACTCC CACAGACCTT CCAGACACCAGACAGACAGACAGACAGACAGACAGACAG											
78 GAGAGAGGG GGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCT CCTCAAGAAC 80 CTGGACCGGC TGAAGCCCGC CATCCGGAGA AAGATCCTGG CCCAATGGA GATCTGAAG 81 CTGGACCGGC TGAAGCCCGC CATCCGGAGA AAGATCCTGG CCCAATGGA CATCTGAAGA 82 CTCTCCTCGGA ACTGGCCAA GAGGTTTAGG GACCTTCCCC TGGAGGTGGA CTTGGCCAAA 83 AGGCGGAGG CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA CTTGGCCAGA 84 AGGCGGAGG CCGACCGGGA GAGGCTTAGG GCCTTTCTGC AGAGGCTGAGC CCCTGGCCC 85 CTCTCCACG AGTTCGGCCT TGTGGAAAGC GCCTTGCGCCC TGGAGGAGG CCCCTGGCCC 86 CTCTCTCAGG ACTCGAAGGA GGCCTTGTGT GGGTTCACC GGGCCCCCA GGCCCCCA GCCTTATAAA 86 CCGCCTAGGG ACTCGAGGAGGGC CCGGGCCCCA AGGACCCAT GTGGCCAT 87 CTTGGCCC TGGCAGGGGGGC CCGGGCGCC AAGACCCTGA CGTTTTGGCCAG 87 CTGAGGGAG GCCTTGAAGGA GGCGCGGGG CTTCTTGCCAA AGACCCTGG CGTTTTGGCC 87 CTGAGGAGA GCCTTGAAGCA GGCCCGGC GACGACCCCA TGCTCCTGG CTACCTCTG 88 CAGCCTTCCA ACACCACCC CCAGGGGGGG CTTCTTCGCAA AGACCTGG CTACCTCTG 89 CAGCGGGGAG ACGACCCCC CTTTCCCAG AGGCCCCA GCCCGCCTT 100 GAGGGGGAGG ACGGGCCCC CCTTTTCCCAG AGGCCCCTG CCAACCTGG CGAGCCCC 100 CAGGGGGAGG AGAGGCCCAC CTTTTCCCAG AGGCCCCAG GCCCACCTTCCAG CCAACCTGC CTACCTCCTC 100 CAGGGCCACA TGCAGGCCAA GGGGGTTGCC CTGACCTGG CCTATCTCAG GCCTTTCCC TACCCAGCCAC TGCAGGCCAC TGCCTGCAG CTTCTCCAG GCCAGCCCAC TCCCACCCCC CTTCAACCCCCC CAACCCCCCC TGCAGCCAG GCCCACCC CAACCCCCC TGCAGCCAG GCCCACCC CAACCCCCC CAACCCCCC TTCAACCCACC CAACCCCCC TTCAACCCACC CAACCCCCC CAACCCCCC TTCAACCACCC CAACCCCCC TTCAACCACCC CAACCCCAC CAACCCCCC TTCAACCACCC CAACCCCACC CAACCCCCCC TTCAACCACC CAACCCCACC CAACCCACC CAACCCCACC CAACCCCACC CAACCCCACC CAACCCCACCC CAACCCCACC CAACCCACC CAACCCACCC CAACCCACCC CAACCCCACCC CAACCCACCC CAACCCACCC CAACCCACCC CAACCCACCC CAACCCACCC CAACCCACCC CAACCCACCA											
TOTAGACCGCC TRANSCOCCC CATCCGGAA AGATCTGG CCCATGATGA CATTCTAAAA 780 TOTAGACCGCC TCTCCTGGA ACCTGCCCAA AGACCTGCCCC TGGAGGTGGA CTTCGCCAAA 780 TOTAGACCGCC TCTCCCCCCC AGACCGGAA GAGCCTTAGG GCCTTTCTGA AGAGCCTTAG GTTTGGCACC AGACCGCCAAGCCC TGGAGGTGGA CTTCGCCAAAA 780 TOTAGACCCC TCTCCCACCGCCC CAGAGCCCT TCTGGAAAGC CCCAAGGCCC TGGAGCAGCCC TGGACCCCCC CAGAGCCCCT TCTCGCCCAAGCCC TGGACCCCCC TGGACCCCCC CAGAGGCCCCCCCC CAGAGGCCCCCCCCC											
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90 CTTCTGGCCC TGGCGGCGC CAGGGGGGC CGGTTCTCCCA AGACCTGAA GCTTATAAA 1020 92 GCCTCAGGG ACCTGAAGGA GGCGGGGG CTTCTCGCCA AAGACCTGAA CGTTCTGGCC 1080 94 CTGAGGGAAG GCCTTGGCCT CCCGCCCGGC GACGACCCCA TGCTCCTCCC CTACCTCCTG 1140 95 GACCCTTCCA ACACCACCCC CGAGGGGTG GCCGGGGCT AGGGCGGGA GTGGACGGAG 1200 98 GAGGGGGGAG AGAGGCCCCC TTTCCGAA AGGCTCTTC CCAACCTGTG GGGAGGCTT 1260 100 GAGGGGGAGG AGAGGCTCCT TTCGGAA AGGCTCTTC CCAACCTGTG GGGAAGGCTT 1260 101 GAGGGGGAGG AGAGGCTCCT TTGCGTTTAC CGGGAGGTG AGAGGCCCCT TTCCGCTGTC 1320 102 CTGGCCACA TGGAGGCAC GGGGGTGCCC CTGGAAGGTG CCTATCTCAC GGCCTTTCCC 104 CTGGAGGTGG CCCAAGGAGAT CGCCCCGCCT GAGGCCGAG TCTTCCGCT GGCCGCCAC 1440 105 CCCTTCAACC TCAACCTCCC GACCCAGCT GAAAGGGTCC TCTTTTGACGA GCTAAGGCTT 1500 106 CCCTTCAACC TCAACCTCCC GACCAGCT GAAAGGGTCC TCTTTGAACGA GCTAAGGCTT 1500 107 GCCCTCCGC AGGCCCACC CATCGTGGAA AAAGGGTCC TCTTTGAACGA GCTAAGGCTT 1500 110 GCCCTCCGCA AGGCCACCC CATCGTGGAA AAGATCCTGC AGCACCAGA GGGCCGCCT 1620 111 CTCAAAGAACA CCCCACCC CATCGTGAA AAGATCTGC ACCACAGAG GCTCACCAAA 1620 112 CTGAAGAACA CCCCCTTGCC GACCCCACC AGGGCAGGC TAACTAGCTC ACCACAGA GGGCCGCCT 1630 113 GAGGAGGGGT GGCCTTCGG GACCCAGCC ACCCCGCT TGGAAGAA TCCCCCAGCA GGGCCAGCC TTCACCAAA 1620 114 CACACCCCCT TCAACCAGAA CCTGATCCG GCCCCTGGAC TAAGAAGGTC GGTCCTGCC 1800 118 GAGGAGGGGG GGCAAGAA CCTGATCGG GCCCTGGAC TAAGAAGGTC GGTCCTCCC GAGGACACC CCCCCTT GAGGAAGAA TCCCCCAGCA GGCCCACCC CACCCCCTT TAACAAGACC TCCCTTACGA GGCCCCACC TTCCCAAC 1920 122 GAGACCCCA GCTGGATTT CGGCGTCCC CGGGAGGCC TAGACCACC 1920 123 CACCTCTCCG GCCACGAAA CCTGATCCGC TTCCCAAG AGGGCCGGA CATCCACACG 1920 124 GCGCCAAGA CCATCAACTT CGGGGTCCT TAAGGCCAAC TCGGCCCCC CCTTCCCCA 1930 125 GAGACCCCT TCCGCAAGAAAC CCTGAAGAACC TCGGCCCCC TCGCTACTC CACACCACG TCCTTCCCAA 1920 126 GAGACCCCT TCCGGAT TGAAGAAGCC TCGGAGGAGG GCGGTACTT TCAAGAGCTC 1920 127 CGGAGGGGG CCAAGGAGAAAA ACCTGAAAAAAAAACC CTGGAGGAGG GAAAGACGCC CACCTCCCAAAAAAAAACCC CAGCCACCC CACCTACGTC CACACCACAAAAAAAAACCC CAGCAAGAGAGCAAAAAAAA											
92 GCCCTCAGGG ACCTGAAGGA GGCGCGGGG CTTCTCGCCA AACACCTGAC CTTCTGGCC 1140 94 CTGAGGGAAG GCCTTGGCT CCCGCCCGGC GACGACCCCA TGCTCCTCCT CTACCTCCTG 95 GACCCTTCCA ACACCACCCC CGAGGGGGT GCCGGGGGT ACGGCGGGGG TGGAGGAGG 96 GAGGCGGGG ACCGGGCCC CCTTTCCGAG AGGCTCTTG CCAACCTGTG GGGAGGCTT 100 GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGAGGTGG AGAGCCCCT TTCCGTGTC 1320 101 CTGGAGGGCAC GGGGGTGCCC CGTGTCGAG GGGCGAGGCTT 1320 102 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCGGGG TCTTCCGCTGTC 1330 104 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAG CTTTTCCAGC GGCCGGCCAC 1440 106 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTTACACCA GGCCTGGGCTA 107 CCCCCTCCGC GCAACACGGA GAAGACCGC AAGACCGCC ACGCCCCCC CTCCTGGGA 1560 108 CCCCTCCCGC GAGCACACGA GAAGACCGC AAGACCGCC ACCCCCCCC											
94 CTGAGGGAAG GCCTTGGCCT CCCGCCCGGC GACGACCCCA TGCTCCTGC CTACCTCCTG 96 GACCCTTCCA ACACCACCC CAGGGGGTG GCCCGGCGCT ACGGCGGGA GTGGACCGAG 98 GAGGGGGGGA AGGGGCCCC CCTTTCCGAC AGGCTCTTGC CCCAACCTGTG GGGAGGCTT 1260 100 GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGGA GAGGCCCCT TTCCGCTGTC 11320 102 CTGGCCCACA TGGAGGCCAC GGGGGTGCGC CTGACCTGTG GGCCGGCCAC 1140 104 CTGGAGGTGG CCGAGGAGAT CGCCCGCCCTC GAGGCCGAGG TCTTCCCCCT GGCCGCCAC 105 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAGAGGTCC TCTTTCACAC GCCCTTGCCC 106 CCCTTCAACC TCAACTCCCG GACCAGCTG GAAGACCGC AGCCGCCAC CTCCTGGAG 110 GCCCTCCGCG GCACCACC CATCGTGGAG AAGACCGCC AGCCGCCCC CGTCCTGGAG 110 GCCCTCCGCG AGGCCCACC CATCGTGGAG AAGACCGCC AAGCCGCCCC CGTCCTGGAG 111 CACACCCCGCT TCAACCAGAC GGCCACCC CATCGTGGAG AAGACCGCC AAGCCGCCCC CGTCCTGGAG 112 CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTACTCC ACCCCAGGAC GGCCCCCC CTCCTGAG 114 CACACCCGCT TCAACCAGAC GGCCACGCC ACGGGCAGC TAAGTACCTC ACCCCAGGAC GGCCCCCC CTCCTGCAC 115 CTCCAGAACA TCCCCGTCCG CACCCGCTT GGGCAGAGAC TCCCCCGGCC CTCATCCC 116 CTCCAGAACA TCCCCGTCCG CACCCGCTT GGGCAGAGAC TCCCCCGGCC CTCATCCCC 118 GAGGAGGGT GGCTATTGGT GGCCTGCAC TATACCCACA AGGGGCGGAGA CATCCACACG 1920 122 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATGCCCC 1860 120 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGCGGAGA CATCCACCG 1920 122 GAGACCGCCA GCTGGATTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCC CTCTCCCAG 2040 124 GCGCCAAGGA CCATCAACTT CGGCGTCCCC CGGGAGGCCG GGGTACGTC 2040 125 GAGACCCCCT TCGGCCGGCG CCGCTACAGG GCCTTCATTG ACCGCTACTT TCAGACCTTC 2040 126 GAGCTAGCCA TCCCTTACGA GAGAGCCCCAG GCCTTCATTG ACGCCACC CCTCTCCCAG 2040 127 GGGGAGGCG CGGCCGGAGGCAT GGCCTTCATAC ACGCCCACC CCTCTCCCAG 2040 128 CCCAAGGTCC CGGCCCGCCGCCCCC CCGTACCTG CCGCCCCC CCTCTCCCAG 2040 129 GAGACCCCTT TCGGCCGCG CCGTTACTG CCGAGAGCCG GGGTACGTC 2280 120 GAGACCCCTT TCGGCCGCG CCGTTCATC CCGAGGCGGA AAGACCCCC CCCCAACGCCC CCCCAACGCCT 2280 124 GGGCAGGCCA AGGAGGCTA GGCCTTCAAC AGGCCTCAC AGGGGGGG GCCGTGGCC CCGCACCTC CCGCACCCC CCGCACCTC CCGCCCCC CCGCACCTC CCGCCCCC CCGCACCTC CCGCACCTC CCGCCCC CCGCACCCC CCGCACCCC CCGCACCTC CCCCCCCC CCGCACC											
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106 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT 108 CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCGCC CGTCCTGGAG 110 GCCCTCCGCG AGGCCCACCC CATCGTGGAG AAGATCCTGC AGTACCGGGA GCTCACCAAG 111 CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC 112 CTGAAGACA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC 114 CACACCCGCT TCAACCAGAC GGCCACGCC ACGGCAGGC TAAGTAGCTC CGATCCCAAC 115 CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGCC CTTCATCGCC 118 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TCCGCCGGC CTTCATCGCC 118 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCCA GGGCTGCCCA 118 GAGGAGGGGT GGCTATTGGT GGCCTCGGAC TATAGCCAGA TAGAGCTCCAG GGTGCTGGCC 120 CACCTCTCCC GCGACGAGAA CCTGATCCCG GTCTTCCAGG AGGGCCGGGGA CATCCACACC 121 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCC TGGACCCCC GATGCGCCCGG 122 GAGACCGCCA GCTGGATGTT CGGCGTCCC CGGGAGGCCC TGGACCCCC GATGCGCCCGG 123 GGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACC CCTCTCCCAG 124 GCGGCCAAGA CCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGACCTTC 125 CGCAAGGTC CGGCCTGGAT TCAGAACACC CTGGAGCAGG CGAGAGGGC GGGTACTC 126 GAGCCTCT TCGGCCGCC CCCTACCGTG CCAGACCTAC AGGCCCAGCG GGGTACTC 127 CGGAGGGCG CCCAGCGCAT GGCCTTCAAC ATGCCCCTC AGGGCACCGC CGCCCACCTC 128 CCGGAGGCGC CCCAGCGCAT GCCCTTCAAC ATGCCCCTC AGGGCACCGC CGCCCACCTC 128 CCGGAGGCCG CCCAAGCGCT GGCCTTCAAC ATGCCCCTC AGGGCACCGC CGCCCACCTC 128 CCGGAGGCCC AGGAGTCAT GGAGGGGGT TATCCCCTCA AGGGCCGGACCCC CGCCCACCTC 128 CCGCAGCCCA AGGAGGTCAT GGAGGGGGT TATCCCCTCAG CCGTGCCCC GGAGGTGGC 120 CTGCGCGCACCAC GGCGCACCCC AAGGAGGTGAT ACCACC 120 CTGCGGGGATAG GGGAGGCCAG GGCCTACCAC AGGAGGGCG CCGGCCCACCAC 121 (i) SEQUENCE CHARACTERISTICS: 14 (i) SEQUENCE CHARACTERISTICS: 15 ATGCCGCGC CCCCCCCCCCCCCCCCCCCCCCCCCCCCC	102 CTGGCCCACA TGGAGGCCAC GGGGGTGCGC CTGGACGTGG CC	TATCTCAG GGCCTTGTCC 1380									
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112 CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC 114 CACACCCGCT TCAACCAGAC GGCCAACGGC ACGGGCAGCC TAAGTAGCTC CGATCCCAAC 116 CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGCCAGAGGA TCCGCCGGGC CTTCATCGCC 118 GAGGAGGGT GGCTATTGGT GGCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 118 GAGGAGGGT GGCTATTGGT GGCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 120 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGA CATCCACACG 1212 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATGCGCCGG 124 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACCG CCTTCCCAG 125 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTT AGCCCTACTT TCAGAGCTTC 126 CCCAAGGTGC GGCCTGGAT TGACAAGACC CTGGAGGAGG GCAGGAGGCG GGGTACCTC 127 CGGGAGCCC CCGCTACGTG CCAGACCTAG AGCCCTACTT TCAGAGCTTC 128 CCCAAGGTGC GGCCTGGAT TGACAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 130 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGCCCCGGGT GAAGAGCGTG 131 CGGCGAGCGCG CCGGACGCAT GGCCTTCAAC ATGCCCGTC AGGGCAGGCC CGCCGACCTC 132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACGCC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAG AAATGGGGC CAGGATGCTC 136 CTTCAGGTC ACGACGAGCT GGTCCTCCAC AGGCTGGAG AAATGGGGC CAGGATGCTC 137 CTCAGGTC ACGACGAGCT GGTCCTCCAC AGGAGGTGAA ACCACC 138 CGGCTGCCCA AGGAGGTCAT GGAGGGGGT TATCCCCTGC CAAAAA GACGCCCCT GGAGGTGGAC 140 GTGGGGATAG GGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 141 (i) SEQUENCE CHARACTERISTICS: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 151 (ii) MOLECULE TYPE: DNA (genomic) 152 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 153 ATGGCGATGC CTCCTCTTT TGAGCCCAAA GGCCGGTGC TCCTGGTGGA CGGCCACCAC 156 ATGGCGATAC GGACCTTCTT TGAGCCCAAA GGCCGGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGAGCCCAAA GGCCGCGGC TCCTCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCG CGAACCCGTT											
114 CACACCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC 116 CTCCAGAACA TCCCCGTCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTCATCGCC 11800 118 GAGGAGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 120 CACCTCTCCG GCCAGAGAA CCTGATCCGG GTCTTCCAGG AGGGCGGGA CATCCACACG 122 GAGACCGCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCC TGGACCCCCT GATGGGCCGG 124 GCGGCCAAGA CCATCAACTT CGGGGTCCCC CGGGAGGCCC TGGACCCCCT GATGGGCCGG 125 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 127 CCCAAGGTCC GGGCCTGGAT TCAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTT 130 GAGACCCTCT TCGGCCGCCC CCGCTACGTG CCAGACCTAA AGCCCCGCG GAAGAGCGTG 132 CGGGAGGCG CCGACGCAT GGCCTTCAAC ATGCCCGTCC AGGGCCACGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGACG AAATGGGGGC CGCCGACCTC 135 CGGCTGGCCA AGGAGGATCT GGTCCTCGAG GCCCCAAAAA AGAGGGCCG CGCCGACCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAA AGAGGGCGGA GGCCGTGGCC 140 GTGGGGATAG GGGAGGACT GGTCCTCGAG GCCCCAAAAA AGAGGGCGGA GGCCGTGGCC 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGATGAT ACCACC 141 (1) SEQUENCE CHARACTERISTICS: 144 (1) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 155 ATGGCGATGC TCCCCTCTT TGAGCCCAAAA GGCCGCGGC CCCAACCCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GCCCTCACCA CCAGCCGCGC CGAACCCGT 120											
116 CTCCAGAACA TCCCCGTCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTCATCGCC 118 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 120 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACACG 121 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATCCGCCGGG 124 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCACCG CCTCTCCCAG 126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTA AGCGCACCC CCTCTCCCAG 127 CCAAAGGTC GGGCCTGGAT TAAGAAGACC CTGGAGGAGG GCAGAAGAGC GGGGTACGTC 128 CCCAAAGGTC GGGCCTGGAT TAAGAAGACC CTGGAGAGG GCAGAAGAGC GGGGTACGTC 130 GAGACCCTCT TCGGCCGCC CCGCTACGTG CCAGACCTAG AGGCCCACG GGGGTACGTC 131 CAGAAGGCG CCGAGCGCAT GGCCTTCAACA ATGCCCGTCC AGGCCCGC CGCCGACCTC 132 CGGGAGGCG CCGAGCGCAT GGCCTTCACA ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTG CTATGGTGAA GCTCTTCCCC AGGCTGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACCAGCT GGTCCTCCGC AGGCTGAGAAAA AGAGGGCGGA GGCCGTGGCC 137 CTGCGCCCA AGGAGGTCAT GGAGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAC 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 141 (1) SEQUENCE CHARACTERISTICS: 142 (1) SEQUENCE CHARACTERISTICS: 143 (1) SEQUENCE CHARACTERISTICS: 144 (1) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 155 ATGGCGTACC GCACCTTCTT TGGCCCCAAA GGCCGCTGC CCCAGCCCGC CGAACCCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGC CGAACCCGTT 120											
118 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 120 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACACG 122 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATGCGCCG 124 GCGGCCAAGA CCATCAACTT CGGGGTCCCC TACGGCATGT CGGCCCACCG CCTCTCCCAG 126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 128 CCCAAGGTGC GGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGTACCTG 130 GAGACCCTCT TCGGCCGCC CCGCTACGTG CCAGACCTAG AGGCCCAGCG GGGTACCTG 131 CGGGAGGCG CCGACCGCA CCCCTCCAACA AGGCCCGGGT GAAGAGCCTC 132 CGGGAGGCG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGGAG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGT GGTCCTCCGC AGGCTGGAGA AAATGGGGGC CAGGATGCTC 137 CGGCTGGCCA AGGAGGTCAT GGAGGGGGT TATCCCCTGG CCGTGCCCCT GGAGGTGGAC 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 141 (i) SEQUENCE CHARACTERISTICS: 142 (i) SEQUENCE CHARACTERISTICS: 143 (I) SEQUENCE CHARACTERISTICS: 144 (I) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 155 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC CCACCTTCTT TGCCCTCAAA GGCCCGCGC CGAACCCGT CACACCC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAA GGCCCGCGC CCACCCCC CACACCCCC CACACCCCCCCC											
120 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACACG 122 GAGACCGCA GCTGGATGTT CGGCGTCCC CGGGAGGCCG TGGACCCCT GATGCGCCGG 124 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG 126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 127 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 130 GAGACCCTCT TCGGCCGCC CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGCCACGGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAG AAATGGGGGC CGGCCACCTC 136 CTTCAGGTCC ACGACCAGCT GGTCCTCCACA AGGCCAGGAG GCCGTGCCC 137 CGGCTGGCCA AGGAGGTCAT GGAGGGGGG GCCCCAAAAG AGAGGGCGGA GGCCGTGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 141 (i) SEQUENCE CHARACTERISTICS: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCG CGAACCCGTT 120											
122 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATGCGCCGG 124 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG 126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 128 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 130 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGACCGTG 132 CGGGAGGCGG CCGACGCAT GGCCTTCAAC ATGCCCGTC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAA AGGAGGGCC CAGGATGCTC 137 CTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAA AGGAGGGCGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGT TATCCCCTGG CCGTGCCCCT GGAGGTGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGATGAT ACCACC 141 (i) SEQUENCE CHARACTERISTICS: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
124 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG 126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 128 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 130 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 142 (2) INFORMATION FOR SEQ ID NO: 2: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
126 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 128 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 130 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAC 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 141 (i) SEQUENCE CHARACTERISTICS: 142 (i) SEQUENCE CHARACTERISTICS: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC CGAACCCGTT 120											
128 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGAGG GCAGGAGGCG GGGGTACGTG 130 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 142 (2) INFORMATION FOR SEQ ID NO: 2: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
130 GAGACCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 142 (2) INFORMATION FOR SEQ ID NO: 2: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 142 (2) INFORMATION FOR SEQ ID NO: 2: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
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136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 142 (2) INFORMATION FOR SEQ ID NO: 2: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 155 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 2506 142 (2) INFORMATION FOR SEQ ID NO: 2: 144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
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144 (i) SEQUENCE CHARACTERISTICS: 145 (A) LENGTH: 2496 base pairs 146 (B) TYPE: nucleic acid 147 (C) STRANDEDNESS: double 148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120		Z300									
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148 (D) TOPOLOGY: linear 150 (ii) MOLECULE TYPE: DNA (genomic) 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120	· ·										
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156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 60 158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120											
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Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\06212002\I940925A.raw

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164		GGGCCCCCAC					300				
166		TCCTAGGCCT					360				
		TGGCCAAGCG					420				
170	GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480				
172		CGGCGTGGCT	TTACGAGAAG		GCCCGGAGCA		540				
174		TGGCGGGGGA					600				
		AGAGGCTCAT					660				
178		AGCCCTCCTT					720				
180	TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCCTGG	AGGTGGACTT	CGGGAGGCGC	780				
182		ACCTGGAGGG		TTTTTGGAGC			840				
184	CTCCACGAGT	TCGGCCTCCT	GGAGGGGCCG	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900				
186	CCGGAAGGGG	CTTTTTTGGG	CTTTTCCTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960				
188	CTGGCCCTGG	CTGGGGCGTG	GGAGGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020				
190	CTGAGGGACC	TTAAGGGGGT	GCGGGGAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080				
192	CGGGAGGGCC	TGGACCTCTT	CCCAGAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140				
		CCACCCTGA					1200				
196	GCGGGGGAGA	GGGCCCTCCT	GGCCGAGCGC	CTCTTCCAGA	CCCTAAAGGA	GCGCCTTAAG	1260				
198	GGAGAAGAAC	GCCTGCTTTG	GCTTTACGAG	GAGGTGGAGA	AGCCGCTTTC	CCGGGTGTTG	1320				
		AGGCCACGGG		GACGTGGCCT			1380				
202	GAGGTGGAGG	CGGAGGTGCG	CCAGCTGGAG	GAGGAGGTCT	TCCGCCTGGC	CGGCCACCCC	1440				
204		ACTCCCGCGA					1500				
206		AGACGGAGAA					1560				
		CCCACCCCAT					1620				
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		ACCAGACGGC					1740				
		CCGTGCGCAC					1800				
		TGCTGGTGGT					1860				
		ACGAGAACCT			GGAGGGACAT		1920				
		GGATGTTCGG		GAAGGGGTAG			1980				
		TCAACTTCGG					2040				
224		CCTACGAGGA			GCTACTTCCA		2100				
		CCTGGATTGA					2160				
		GCCGCCGGCG					2220				
		AGCGCATGGC					2280				
232		TGGTGCGGCT					2340				
234		ACGAGCTGGT					2400				
236		AGGTCATGGA					2460				
		AGGACTGGCT					2496				
242	240 (2) INFORMATION FOR SEQ ID NO: 3: 242 (i) SEQUENCE CHARACTERISTICS:										
243	, ,										
244	· · · · · · · · · · · · · · · · · · ·										
245	· ·										
246	, ,										
248		OLECULE TYP		omic)							
252		EQUENCE DES			:		-				
	ATGGAGGCGA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	тсстсстсст	GGACGGCCAC	60				
		ACCGCACCTT					120				
230	CACCIGGCCI	ccccaccii	2110000010		-0						

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\06212002\1940925A.raw

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258 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC
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260 AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG
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262 GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC
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264 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC
                                                                         360
                                                                         420
266 GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC
268 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG
                                                                         480
270 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG
                                                                         540
272 GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC
                                                                         600
274 GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG
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276 AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC
                                                                         720
278 CTCAGGCTCT CCTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC
                                                                         780
280 GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC
                                                                         840
                                                                         900
282 GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCTGGA GGAGGCCCCC
284 TGGCCCCCGC CGGAAGGGC CTTCGTGGC TTCGTCCTCT CCCGCCCCGA GCCCATGTGG
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286 GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC
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288 TTGGCGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC
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290 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC
                                                                        1140
292 CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GGCGCTACGG GGGGAGTGG
                                                                        1200
294 ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG
296 CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC
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298 CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC
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300 CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG
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302 GGCCACCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT
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304 AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG
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306 CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC
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308 ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC
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310 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC
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312 CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC
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314 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC
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316 CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC
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318 CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG
                                                                        1980
320 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC
                                                                         2040
322 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA
2160
326 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA
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328 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG
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330 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCGCA
                                                                        2340
332 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG
                                                                         2400
334 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG
                                                                         2460
336 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG
                                                                         2504
338 (2) INFORMATION FOR SEQ ID NO: 4:
         (i) SEQUENCE CHARACTERISTICS:
340
341
              (A) LENGTH: 832 amino acids
342
              (B) TYPE: amino acid
343
              (C) STRANDEDNESS: single
344
              (D) TOPOLOGY: linear
346
        (ii) MOLECULE TYPE: protein
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
350
352
        Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
```

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\06212002\1940925A.raw

353	1				5		•			10					15	
	_	200	C1 **	uic	-	Tou	λla	Пиг	λra		Dhe	Hie	λla	T.a.ı		Gly
355	val	ASP	GIY	20	птъ	ьеu	ALG	TYT	25	1111	riic	1113	AIG	30	цуз	GLI
356	T	mh	Thr		7 ~~	C1	C3.11	Dro		Cln	λla	Val	Фиг		Dhe	λla
358	ьeu	THE		261	Arg	GIY	GIU	40	Vai	GIII	ALG	Val	45	GLY	FIIC	ΑIα
359	T	C	35	*	T		T		C1	200	C1	A an		Va I	T10	Val
361	гÀг		Leu	Leu	гаг	Ala		тÃг	GIU	ASP	GIY	60	нта	vai	116	Val
362		50	_				55	a	D1	3	774 -		31-	M	C1	C1
364		Phe	Asp	Ala	ьys		Pro			Arg		GIU	Ala	TAL	GIY	
365	65	_			_	70	_			a 1 .	75	D1	D		a1	80
367	Tyr	Lys	Ala	GIĀ		Ala	Pro	Thr	Pro		Asp	Pne	Pro	Arg		ьeu
368		_		_	85	_		_	_	90	-	-			95	~1
370	Ala	Leu	Ile	_	Glu	Leu	val	Asp		ьeu	GIY	ьeu	АТА		Leu	GIU
371			_	100	_			_	105	_		_	_	110	_	_
373	Val	Pro	Gly	Tyr	Glu	Ala	Asp		Val	Leu	Ala	Ser		Ala	Lys	гāг
374			115					120		_			125			_
376	Ala	Glu	Lys	Glu	Gly	Tyr		Val	Arg	Ile	Leu		Ala	Asp	Lys	Asp
377		130					135					140				
379	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
380	145				•	150					155					160
382	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	\mathtt{Trp}	Glu	Lys	Tyr	Gly	Leu	Arg	Pro
383					165					170					175	
385	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn
386				180					185					190		
388	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu
389			195					200					205			
391	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu
392		210					215					220				
394	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys
395	225					230					235					240
397	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val
398					245			•		250					255	
400	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe
401	_			260					265					270		
403	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
404			275				_	280					285			
406	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
407		290		-			295				_	300				
409	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp
410	305			•		310			-	_	315					320
412		Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly		Val	His	Arg	Ala	Pro
413					325				-	330	-			-	335	
415	Glu	Pro	Tvr	Lvs		Leu	Arq	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu
416			- 4	340			_	•	345				_	350		
418	Ala	Lvs	Asp		Ser	Val	Leu	Ala			Glu	Gly	Leu	Gly	Leu	Pro
419		-1-	355					360		,		-	365	_		
421	Pro	Glv		Asp	Pro	Met	Leu		Ala	Tvr	Leu	Leu		Pro	Ser	Asn
422		370					375			-1-		380				
424	Thr		Pro	Glu	Glv	Val			Ara	Tvr	Glv		Glu	Trp	Thr	Glu
425	385		0	u	~_1	390		9	9	-1-	395	1				400
723	505					220										